

Title	High-quality draft genome sequence of <i>Bifidobacterium longum</i> E18, isolated from a healthy adult
Authors	Zhurina, Daria;Dudnik, Alexey;Waidmann, Mark S.;Grimm, Verena;Westermann, Christina;Breitinger, Katrin J.;Yuan, Jing;van Sinderen, Douwe;Riedel, Christian U.
Publication date	2013-12
Original Citation	Zhurina, D., Dudnik, A., Waidmann, M. S., Grimm, V., Westermann, C., Breitinger, K. J., Yuan, J., van Sinderen, D. and Riedel, C. U. (2013) 'High-Quality Draft Genome Sequence of <i>Bifidobacterium longum</i> E18, Isolated from a Healthy Adult', <i>Genome Announcements</i> , 1(6). doi: 10.1128/genomeA.01084-13
Type of publication	Article (peer-reviewed)
Link to publisher's version	10.1128/genomeA.01084-13
Rights	© 2013 Zhurina et al. This is an open-access article distributed under the terms of the Creative Commons Attribution 3.0 Unported license. - https://creativecommons.org/licenses/by/3.0/
Download date	2024-05-21 23:58:55
Item downloaded from	https://hdl.handle.net/10468/3446



UCC

University College Cork, Ireland
Coláiste na hOllscoile Corcaigh

High-Quality Draft Genome Sequence of *Bifidobacterium longum* E18, Isolated from a Healthy Adult

Daria Zhurina,^a Alexey Dudnik,^b Mark S. Waidmann,^a Verena Grimm,^a Christina Westermann,^a Katrin J. Breitingner,^a Jing Yuan,^c Douwe van Sinderen,^d Christian U. Riedel^a

Institute of Microbiology and Biotechnology, University of Ulm, Ulm, Germany^a; Institute of Plant Biology, University of Zurich, Zurich, Switzerland^b; Institute of Disease Control and Prevention, Academy of Military Medical Sciences, Beijing, China^c; Alimentary Pharmabiotic Centre and Department of Microbiology, Biosciences Institute, University College Cork, Cork, Ireland^d

Bifidobacteria are important gastrointestinal commensals of a number of animals, including humans, and various beneficial effects on host health have been attributed to them. Here, we announce the noncontiguous finished genome sequence of *Bifidobacterium longum* E18, isolated from a healthy adult, which reveals traits involved in its interaction with the host.

Received 15 November 2013 Accepted 26 November 2013 Published 19 December 2013

Citation Zhurina D, Dudnik A, Waidmann MS, Grimm V, Westermann C, Breitingner KJ, Yuan J, van Sinderen D, Riedel CU. 2013. High-quality draft genome sequence of *Bifidobacterium longum* E18, isolated from a healthy adult. *Genome Announc.* 1(6):e01084-13. doi:10.1128/genomeA.01084-13.

Copyright © 2013 Zhurina et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 3.0 Unported license](http://creativecommons.org/licenses/by/3.0/).

Address correspondence to Christian U. Riedel, christian.riedel@uni-ulm.de.

Bifidobacteria are considered to be GRAS (generally recognized as safe) microorganisms that are widely used as probiotics. Probiotics are defined as live microbial food supplements that have a beneficial effect on host health when administered in adequate amounts (1). The beneficial effects of bifidobacteria have been studied mainly in animal models and include immune modulation, pathogen inhibition, and the alleviation of intestinal inflammation (2–7). Genome sequencing and analysis of members of the genus *Bifidobacterium* are powerful approaches to identify the genetic determinants involved in the interaction with the host. To extend knowledge of this subject, we have sequenced the genome of the commensal *B. longum* E18 strain, which was isolated from the feces of a healthy adult.

A 7.9-kb paired-end library was constructed and sequenced using a Roche Genome Sequencer FLX Titanium platform by a commercial sequencing service provider, Eurofins MWG Operon (Ebersberg, Germany). A total of 246,462 individual quality-filtered reads comprising 53,491,261 bp were obtained, resulting in a 26.7-fold average coverage. The read sequences were assembled using Newbler 2.3 and Staden package 2.0.0b9 into six contigs put together into one megascaffold. Initial tRNA, rRNA, and open reading frame (ORF) prediction and functional annotation were done using the RAST server (8). The translational start sites of automatically annotated ORFs were manually corrected using Artemis software (9) based on the positions of potential ribosomal binding sites, the G+C profile, and alignments with homologous ORFs from other organisms. Manual corrections of automatically assigned functions were verified on an individual gene-by-gene basis using BLASTp (10) searches against the nonredundant protein sequence database.

The estimated genome size of strain E18 is 2,372,966 bp, with an average G+C content of 59.96%. The genome contains 1,862 protein-encoding genes, 4 rRNA operons, and an unusually high number of tRNA genes (62 in total). Putative functions were assigned to 1,299 genes (67%). The amino acid sequences

encoded by 99 genes contain putative signal peptide sequences, and thus, these proteins might be secreted via the classical *sec* pathway. *B. longum* E18 harbors a complete *tatABC* secretion system (BLONG_0088-90) and at least 4 of the secreted proteins (BLONG_0091, BLONG_0223, BLONG_0425, and BLONG_1620) are predicted to be exported via this pathway. Approximately half of all secreted proteins are predicted hydrolases, substrate binding proteins, and components of transport systems with a putative role in the acquisition of nutrients, which represents an adaptation of bifidobacteria to the gastrointestinal habitat (11–13). Further genes with a potential role in interaction with the host carried in the *B. longum* E18 genome include two putative exopolysaccharide (EPS) biosynthesis gene clusters (BLONG_0398-0417 and BLONG_2008-2021) and a gene cluster encoding Tad pili (BLONG_0140-0145). Both traits were previously shown to be important for *in vivo* colonization and modulation of the immune system by bifidobacteria (2, 14).

Nucleotide sequence accession numbers. The genome sequence of *B. longum* E18 has been deposited at DDBJ/EMBL/GenBank under the accession no. AUYPD00000000. The version described in this paper is version AUYPD01000000. The assigned NCBI taxonomy identification number is 1322347.

ACKNOWLEDGMENTS

C.U.R., D.Z., V.G., and J.Y. were funded by the German Academic Exchange Service and Federal Ministry of Education and Research (grant no. D/09/04778). D.Z. additionally received a Research Prize (Forschungsbonus) of the University of Ulm for this project. A.D. was supported by the Swiss National Science Foundation (grant no. 31003A-134936). D.V.S. was supported by the Science Foundation Ireland (SFI) under grant no. 07/CE/B1368 and SFI/12/RC/2273. C.W. received an LGFG stipend (no. 1215 LGFG-E).

We are grateful to Aldert Zomer (Nijmegen Medical Centre, Netherlands) for help with the initial steps of genome assembly.

REFERENCES

1. Food and Agricultural Organization of the United Nations/World Health Organization. 2011. Guidelines for the evaluation of probiotics in food. Joint FAO/WHO Working Group Meet., London, London Ontario, Canada, 30 April to 1 May 2002.
2. Fanning S, Hall LJ, Cronin M, Zomer A, Macsharry J, Goulding D, O'Connell Motherway M, Shanahan F, Nally K, Dougan G, van Sinderen D. 2012. Bifidobacterial surface-exopolysaccharide facilitates commensal-host interaction through immune modulation and pathogen protection. *Proc. Natl. Acad. Sci. U. S. A.* 109:2108–2113.
3. Fukuda S, Toh H, Hase K, Oshima K, Nakanishi Y, Yoshimura K, Tobe T, Clarke JM, Topping DL, Suzuki T, Taylor TD, Itoh K, Kikuchi J, Morita H, Hattori M, Ohno H. 2011. Bifidobacteria can protect from enteropathogenic infection through production of acetate. *Nature* 469: 543–547.
4. Heuvelin E, Lebreton C, Granelle C, Pot B, Cerf-Bensussan N, Heyman M. 2009. Mechanisms involved in alleviation of intestinal inflammation by *Bifidobacterium breve* soluble factors. *PLoS One* 4:e5184. doi:10.1371/journal.pone.0005184.
5. Jeon SG, Kayama H, Ueda Y, Takahashi T, Asahara T, Tsuji H, Tsuji NM, Kiyono H, Ma JS, Kusu T, Okumura R, Hara H, Yoshida H, Yamamoto M, Nomoto K, Takeda K. 2012. Probiotic *Bifidobacterium breve* induces IL-10-producing Tr1 cells in the colon. *PLOS Pathog.* 8:e1002714. doi:10.1371/journal.ppat.1002714.
6. Preising J, Philippe D, Gleinser M, Wei H, Blum S, Eikmanns BJ, Niess JH, Riedel CU. 2010. Selection of bifidobacteria based on adhesion and anti-inflammatory capacity *in vitro* for amelioration of murine colitis. *Appl. Environ. Microbiol.* 76:3048–3051.
7. Veiga P, Gallini CA, Beal C, Michaud M, Delaney ML, DuBois A, Khlebnikov A, van Hylckama Vlieg JET, Punit S, Glickman JN, Onderdonk A, Glimcher LH, Garrett WS. 2010. *Bifidobacterium animalis* subsp. *lactis* fermented milk product reduces inflammation by altering a niche for colitogenic microbes. *Proc. Natl. Acad. Sci. U. S. A.* 107: 18132–18137.
8. Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formis K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil LK, Paarmann D, Paczian T, Parrello B, Pusch GD, Reich C, Stevens R, Vassieva O, Vonstein V, Wilke A, Zagnitko O. 2008. The RAST server: Rapid Annotations using Subsystems Technology. *BMC Genomics* 9:75. doi:10.1186/1471-2164-9-75.
9. Rutherford K, Parkhill J, Crook J, Horsnell T, Rice P, Rajandream MA, Barrell B. 2000. Artemis: sequence visualization and annotation. *Bioinformatics* 16:944–945.
10. Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ. 1990. Basic local alignment search tool. *J. Mol. Biol.* 215:403–410.
11. Sela DA, Chapman J, Adeuya A, Kim JH, Chen F, Whitehead TR, Lapidus A, Rokhsar DS, Lebrilla CB, German JB, Price NP, Richardson PM, Mills DA. 2008. The genome sequence of *Bifidobacterium longum* subsp. *infantis* reveals adaptations for milk utilization within the infant microbiome. *Proc. Natl. Acad. Sci. U. S. A.* 105:18964–18969.
12. Turroni F, Bottacini F, Foroni E, Mulder I, Kim JH, Zomer A, Sánchez B, Bidossi A, Ferrarini A, Giubellini V, Delledonne M, Henrissat B, Coutinho P, Oggioni M, Fitzgerald GF, Mills D, Margolles A, Kelly D, van Sinderen D, Ventura M. 2010. Genome analysis of *Bifidobacterium bifidum* PRL2010 reveals metabolic pathways for host-derived glycan foraging. *Proc. Natl. Acad. Sci. U. S. A.* 107:19514–19519.
13. Schell MA, Karmirantzou M, Snel B, Vilanova D, Berger B, Pessi G, Zwahlen MC, Desiere F, Bork P, Delley M, Pridmore RD, Arigoni F. 2002. The genome sequence of *Bifidobacterium longum* reflects its adaptation to the human gastrointestinal tract. *Proc. Natl. Acad. Sci. U. S. A.* 99:14422–14427.
14. O'Connell Motherway M, Zomer A, Leahy SC, Reunanen J, Bottacini F, Claesson MJ, O'Brien F, Flynn K, Casey PG, Munoz JA, Kearney B, Houston AM, O'Mahony C, Higgins DG, Shanahan F, Palva A, de Vos WM, Fitzgerald GF, Ventura M, O'Toole PW, van Sinderen D. 2011. Functional genome analysis of *Bifidobacterium breve* UCC2003 reveals type IVb tight adherence (Tad) pili as an essential and conserved host-colonization factor. *Proc. Natl. Acad. Sci. U. S. A.* 108:11217–11222.